

008271-113800

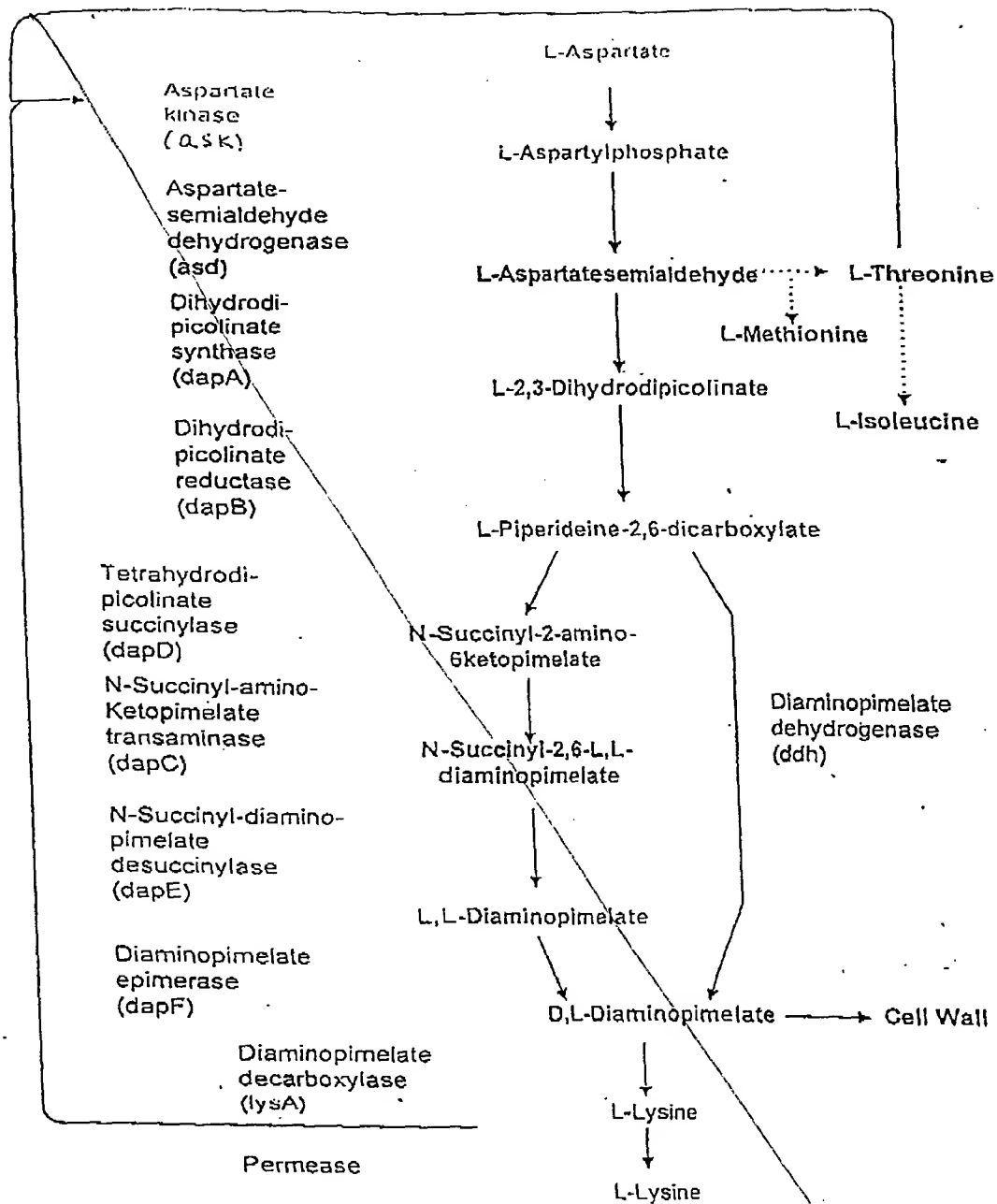


Figure 1

008211-144260

Nucleotide sequence of ATCC21529 ask (SEQ ID NO:1)

```
1 GTGGCCCTGC TCGTACAGAA ATATGGCGGT TCCTCGCTTG AGAGTGC GGA
51 ACGCATTAGA AACGTCGCTG AACGGATCGT TGCCACCAAG AAGGCTGGAA
101 ATGATGTCGT GGTGTCTGC TCCGCAATGG GAGACACCAC GGATGAACCT
151 CTAGAACTTG CAGCGGCAGT GAATCCCGTT CCGCCAGCTC GTGAAATGGA
201 TATGCTCCTG ACTGCTGGTG AGCGTATTTC TAACGCTCTC GTCGCCATGG
251 CTATTGAGTC CCTTGGCGCA GAAGCTCAAT CTTTCACTGG CTCTCAGGCT
301 GGTGTGCTCA CCACCGAGCG CCACGGAAAC GCACGCATTG TTGACGTCAC
351 ACCGGGTCGT GTGCGTGAAG CACTCGATGA GGGCAAGATC TGCATTGTTG
401 CTGGTTTTCA GGGTGTTAAT AAAGAAACCC GCGATGTCAC CACGTTGGGT
451 CGTGGTGGTT CTGACACCAC TGCAGTTGCG TTGGCAGCTG CTTTGAACGC
501 TGATGTGTGT GAGATTTACT CGGACGTTGA CGGTGTGTAT ACCGCTGACC
551 CGCGCATCGT TCCTAATGCA CAGAAGCTGG AAAAGCTCAG CTTTGAAGAA
601 ATGCTGGAAC TTGCTGCTGT TGGCTCCAAG ATTTTGGTGC TCGCGAGTGT
651 TGAATACGCT CGTGCATTCA ATGTGCCACT TCGCGTACGC TCGTCTTATA
701 GTAATGATCC CGGCACTTTG ATTGCCGGCT CTATGGAGGA TATTCCTGTG
751 GAAGAAGCAG TCCTTACCGG TGTGCAACC GACAAGTCCG AAGCCAAAGT
801 AACC GTTCTG GGTATTTCCG ATAAGCCAGG CGAGGCTGCC AAGGTTTTCC
851 GTGCGTTGGC TGATGCAGAA ATCAACATTG ACATGGTTCT GCAGAACGTC
901 TCCTCTGTGG AAGACGGCAC CACCGACATC ACGTTCACCT GCCCTCGCGC
951 TGACGGACGC CGTGCATGG AGATCTTGAA GAAGCTTCAG GTTCAGGGCA
1001 ACTGGACCAA TGTGCTTTAC GACGACCAGG TCGGCAAAGT CTCCCTCGTG
1051 GGTGCTGGCA TGAAGTCTCA CCCAGGTGTT ACCGCAGAGT TCATGGAAGC
1101 TCTGCGCGAT GTCAACGTGA ACATCGAATT GATTTCCATC TCTGAGATCC
1151 GCATTTCCGT GCTGATCCGT GAAGATGATC TGGATGCTGC TGCACGTGCA
1201 TTGCATGAGC AGTTCCAGCT GGGCGGCGAA GACGAAGCCG TCGTTTATGC
1251 AGGCACCGGA CGCTAA
```

Fig. 2

pro amino acid sequence of ATCC 21529 ant:

[illegible]

Fig 3A

290x  
114

[illegible]

Fig. 38

3

Nucleotide.                      sequence of ATCC21529 and (SEQ ID NO:2)

```

1  ATGACCACCA TCGCAGTTGT TGGTGAACC GGCCAGGTCG GCCAGGTTAT
51  GCGCACCTTT TTGGAAGAGC GCAATTCCCC AGCTGACACT GTTCGTTTCT
101 TTGCTTCCCC GCGTTCCGCA GGCCGTAAGA TTGAATTCCG TGGCACGGAA
151 ATCGAGGTAG AAGACATTAC TCAGGCAACC GAGGAGTCCC TCAAGGGCAT
201 CGACGTTGCG TTGTTCTCTG CTGGAGGCAC CGCTTCCAAG CAGTACGCTC
251 CACTGTTTGC TGCTGCAGGC GCGACTGTTG TGGATAACTC TTCTGCTTGG
301 CGCAAGGACG ACGAGGTTCC ACTAATCGTC TCTGAGGTGA ACCCTTCCGA
351 CAAGGATTCG CTGGTCAAGG GCATTATTGC GAATCCTAAC TGCACCACCA
401 TGGCTGCAAT GCCAGTGCTG AAGCCACTGC ACGATGCCGC TGGTCTTGTA
451 AAGCTTCACG TTTCTCTTA CCAGGCTGTT TCCGTTCTG GTCTTGACAG
501 TGTGGAAACC TTGGCAAAGC AGGTTGCTGC AGTGGCGAC CACAACGTTG
551 AGTTCGTCCA TGATGGACAG GCTGCTGACC CAGGCGATGT CGGACCTTAC
601 GTTTCCCCAA TCGCTTACAA CGTGTGCCA TTCGCCGAA ACCTCGTCGA
651 TGACGGCACC TTCGAAACCG ACGAGAGCA GAAGCTGCGC AACGAATCCC
701 GCAAGATTCT CGGCCTCCA GACCTCAAGG TCTCAGGCAC CTGCGTCCGC
751 GTGCCGGTTT TCACCGGCCA CACGCTGACC ATTACGCGG AATTCGACAA
801 GGCATCACC GTCGAGCAGG CGCAGGAGAT CTTGGGTGCC GCTTCAGGCG
851 TCGAGCTTGT CGACGTCCA ACCCCTTGG CAGCTGCCGG CATGACGAA
901 TCCCTCGTTG GACGCATCCG TCAGSACTCC ACTGTCGACC ACAACCGCGG
951 TCTGGTTCTC GTCGTATCTG GCGATAACCT TCGCAAGGGC GCAGCACTGA
1001 ACACCATTCA GATTGCTGAG CTCCTGGTTA AGTAA

```

Fig. 4

SEQ. ID. No: 4 amino acid sequence of ATCC 21529 asd

```

ATGACCACCATCGCAGTTGTTGGTGCACCGGCCAGGTCCGGCCAGGTTATGCCGACCTTT
1 ----- 60
M T T I A V V G A T G Q V G Q V H R T F
TTGGAAGAGCGCAATTTCCGAGCTGACACTGTTGGTTCTTTGCTTCCCCCGTTCCGCA
61 ----- 120
L E E R N F P A D T V R F F A S P R S A
GGCCGTAGATTGAATTCGGTGGCACGGAAATCGAGGTAGAAGACATTACTCAGGCAACC
121 ----- 180
G R K I E F R G T E I E V E D I T O A T
GAGGACTCCCTCAAGGGCATCGACGTTGGTTGTTCTCTGCTGGAGGCACCGCTTCCAA
181 ----- 240
E E S L K G I D V A L F S A G G T A S K
CAGTACGCTCCACTGTTTGGTGGTGGAGGCGGACTGTTGGGATAACCTCTCTGTTGG
241 ----- 300
Q Y A P L F A A A G A T V V D N S S A W
CCCAAGGACGACGAGGTTCCACTAATCGTCTGTGAGGTGAACCGTTCCGACAAAGATTCC
301 ----- 360
R K D D E V P L I V S E V N P S D K D S
CTGGTCAAGGGCATTATTGCGAATCTTAAGTGCACCACTGGCTGCAATGCCAGTGGTG
361 ----- 420
L V K G I I A N P N C T T H A A M P V L
AAGCCACTGCAGGATGCCGCTGGTCTTTGTAAGGCTTCAGGTTTCTCTTACCAGGCTGT
421 ----- 480
K P L K D A A G L V L L R V S S Y Q A V
TCCCGTTCTGGTCTTGCAGGTGTGCAATCTTTGGCAAGCAGGTTGCTGCAATTCGGCAG
481 ----- 540
S G S G L A C V E T L A K Q V A A V G D
CAACACGTTGAGTTGCTCCATGATGGACAGGTTGCTGACGACGCGATGTGGGACCTTAC
541 ----- 600
K N V E F V H D G Q A A D A G D V G P Y
GTTTCCCAATCGCTTACAACGTGCTGCCATTCCCGGAAACCTCGTCGATGACGGCACC
601 ----- 660
V S P I A Y H V L P F A C H L V D U G T
TTCGAAACGACGAAGAGCAGAAGCTGCCAAGCAATCCCGAAGATTCTCGGCTCCCA
661 ----- 720
F E T D E E Q K L R K E S R K I L G L P
GACCTCAAGGTTCTCAGGCACCTCGGTCGGTGGCGGTTTTCACCGGCACACGCTGACC
721 ----- 780
D L K V S G T C V R V P V E T C H T L T
ATTACGCGCAATTGCAACCAATCACCCTGACGACGCGGAGAGATCTTGGGTGCC
781 ----- 840
I H A E F D K A I T V E Q A Q E I L C A
GCTTCAGGCGTTCGAGCTTGTGACGTCCTCAACCCCACTTCCAGCTCCCGCATTCAGCAA
841 ----- 900
A S G V E L V D V S T P L A A A C I O E

```

Fig 5A

SEQ ID NO:4  
(Cont)

```

901  TCCCTCGTTGGACGCATCCGTCAGGACTCCACTGTCGACGACAACCGCGGTCTGGTTCTC
    S L V G R I R Q D S T V D D N R G L V L
961  GTCGTATCTGGCGATAACCTTCGCAAGGGCGCAGCACTGAACACCATTTCAGATTGCTGAG
    V V S G D N L R K G A A L N T I Q I A E
1021 CTGCTGGTTAAGTAA
    L L V K
1035

```

Fig 5B

0972441-112800

Nucleotide.	sequence of	dapA (SEQ ID NO:5)
1	ATGAGCACAG	GTTTAACAGC TAAGACCGGA GTAGAGCACT TCGGCACCGT
51	TGGAGTAGCA	ATGGTTACTC CATTACCGGA ATCCGGAGAC ATCGATATCG
101	CTGCTGGCCG	CGAAGTCGCG GCTTATTGG TTGATAAGGG CTGGGATTCT
151	TTGGTTCTCG	CGGGCACCAC TGGTGAATCC CCAACGACAA CCGCCGCTGA
201	AAACTAGAA	CTGCTCAAGG CCGTTCGTGA GGAAGTTGGG GATCGGGCGA
251	AGCTCATCGC	CGGTGTCGGA ACCAACAACA CGCGGACATC TGTGGAACCT
301	GCGGAAGCTG	CTGCTTCTGC TGGCGCAGAC GGCCTTTTAG TTGTAACCTC
351	TTATTACTCC	AAGCCGAGCC AAGAGGGATT GCTGGCGCAC TTCGGTGCAA
401	TTGCTGCAGC	AACAGAGGTT CCAATTTGTC TCTATGACAT TCCTGGTCGG
451	TCAGGTATTC	CAATTGAATC TGATACCATG AGACGCCTGA GTGAATTACC
501	TACGATTTTG	GCGGTCAAGG ACGCCAAGGG TGACCTCGTT GCAGCCACGT
551	CATTGATCAA	AGAAACGGGA CTTGCCTGGT ATTCAGGCGA TGACCCACTA
601	AACCTTGTTT	GGCTTGCTTT GGGCGGATCA GGTTTCATT CCGTAATTGG
651	ACATGCAGCC	CCCACAGCAT TACGTGAGTT GTACACAAGC TTCGAGGAAG
701	GCGACCTCGT	CCGTGCGCGG GAAATCAACG CCAAACATC ACCGCTGGTA
751	GCTGCCCCAAG	GTCGCTTGGG TGGAGTCAGC TTGGCAAAAG CTGCTCTGCG
801	TCTGCAGGGC	ATCAACGTAG GAGATCCTCG ACTTCCAATT ATGGCTCCAA
851	ATGAGCAGGA	ACTTGAGGCT CTCCGAGAAG ACATGAAAAA AGCTGGAGTT
901	CTATAA	

Fig 6



aa sequence  
of dapt

Fig 7

[illegible]

Nucleotide	sequence of	dapB (SEQ ID NO: 7)
1	ATGGGAATCA	AGGTTGGCGT TCTCGGAGCC AAGGSCCGTG TTGGTCAAAC
51	TATTGTGGCA	GCAGTCAATG AGTCCGACGA TCTGGAGCTT GTTGCAAGAG
101	TCGGCGTCGA	CGATGATTG AGCCTTCTGG TAGACAACGG CGCTGAAGTT
151	GTGCTTGACT	TCACCACTCC TAACGCTGTG ATGGGCAACC TGGAGTTCTG
201	CATCAACAAC	GGCATTCTG CGGTTGTTGG AACCACGGGC TTCGATAATG
251	CTCGTTTGGA	GCAGGTTCCG GcCTGGCTTG AAGGAAAAGA CAATGTCGGT
301	GTTCTGATCG	CACCTAACTT TGCTATCTCT GCGGTGTTGA CCATGGTCTT
351	TTCCAAGCAG	GCTGCCCGCT TCTTCGAATC AGCTGAAGTT ATTGAGCTGC
401	ACCACCCCAA	CAAGCTGGAT GCACCTTCAG GCACCGCGAT CCACACTGCT
451	CAGGGCATTG	CTGCCGCACG CAAAGAAGCA GGCATGGACG CACAGCCAGA
501	TGCGACCGAG	CAGGCACTTG AGGGTTCCCG TGGCGCAAGC GTAGATGGAA
551	TCCCAGTTCA	cGCAGTCCGC ATGTCCGGCA TGGTTGCTCA CGAGCAAGTT
601	ATCTTTGGCA	CCCAGGGTCA GACCTTGACC ATCAAGCAGG ACTCCTATGA
651	TCGCAACTCA	TTTGCACCAG GTGTCTTGGT GGGTGTGCGC AACATTGCAC
701	AGCACCCAGG	CCTAGTCGTA GGACTTGAGC ATTACCTAGG CCTGTAA

Fig 8

008277-1-112800

SEQID NO. 8 Amino acid sequence of dapB

```

1  ATGGGAATCAAGGTTGGCGTTCTCGGAGCCAAAGSCCGTGTGGTCAAACCTATTGTGGCA
   -----+-----+-----+-----+-----+-----+-----+-----+
M  G  I  K  V  G  V  L  G  A  K  G  R  V  G  Q  T  I  V  A
61  GCAGTCAATGAGTCCGACGATCTGGAGCTTGTTCGAGAGATCGGCGTCCGACGATGATTG
   -----+-----+-----+-----+-----+-----+-----+-----+
A  V  N  E  S  D  D  L  E  L  V  A  E  I  G  V  D  D  D  L
121 AGCCTTCTGGTAGACAACGGCGCTGAAGTTGTCGTTGACTTCACCACTCCTAACGCTGTG
   -----+-----+-----+-----+-----+-----+-----+-----+
S  L  L  V  D  N  G  A  E  V  V  V  D  F  T  T  P  N  A  V
181 ATGGGCAACCTGGAGTTCTGCATCAACAACGGCATTCTGCGGTTGTTGGAACACGGGC
   -----+-----+-----+-----+-----+-----+-----+-----+
M  G  N  L  E  F  C  I  N  N  G  I  S  A  V  V  G  T  T  G
241 TTCGATAATGCTCGTTTGGAGCAGGTTCCGCGCTGGCTTGAAGGAAAAGACAATGTCCGT
   -----+-----+-----+-----+-----+-----+-----+-----+
F  D  N  A  R  L  E  Q  V  R  A  W  L  E  G  K  D  N  V  G
301 GTTCTGATCGCACCTAACTTTGCTATCTCTGCGGTGTTGACCATGGTCTTTTCCAAGCAG
   -----+-----+-----+-----+-----+-----+-----+-----+
V  L  I  A  P  N  F  A  I  S  A  V  L  T  M  V  F  S  K  Q
361 GCTGCCCGCTTCTTCGAATCAGCTGAAGTTATTGAGCTGCACCACCCCAACAAGCTGGAT
   -----+-----+-----+-----+-----+-----+-----+-----+
A  A  R  F  F  E  S  A  E  V  I  E  L  H  H  P  N  K  L  D
421 GCACCTTCAGGCACCGCGATCCACACTGCTCAGGGCATGCTGCGGCACGCAAAGAAGCA
   -----+-----+-----+-----+-----+-----+-----+-----+
A  P  S  G  T  A  I  H  T  A  Q  G  I  A  A  A  R  K  E  A
481 GGCATGGACGCACAGCCAGATGCGACCGAGCAGGCACTTGAGGGTTCCCGTGGCGCAAGC
   -----+-----+-----+-----+-----+-----+-----+-----+
G  M  D  A  Q  P  D  A  T  E  Q  A  L  E  G  S  R  G  N  S
541 GTAGATGGAATCCCaGTTCAcGCAGTCCGCATGTCCGGCATGGTTGCTCACGAGCAAGTT
   -----+-----+-----+-----+-----+-----+-----+-----+
V  D  G  I  P  V  H  A  V  R  M  S  G  M  V  A  H  E  Q  V
601 ATCTTTGGCACCCAGGGTCAGACCTTGACCATCAAGCAGGACTCCTATGATCGCAACTCA
   -----+-----+-----+-----+-----+-----+-----+-----+
I  F  G  T  Q  G  Q  T  L  T  I  K  Q  D  S  Y  D  R  N  S
661 TTGCACCAAGGTGTCTTGGTGGGTGTGCGCAACATTGCACAGCACCCAGGCCTAGTCGTA
   -----+-----+-----+-----+-----+-----+-----+-----+
F  A  P  G  V  L  V  G  V  R  N  I  A  Q  H  P  G  L  V  V
721 GGACTTGAGCATTACCTAGGCCTGTAA
   -----+-----+-----+-----+-----+-----+-----+-----+
G  L  E  H  Y  L  G  L  +

```

Fig. 9



SEQ ID 10: amino acid sequence of ddh.

SEQ ID  
NO: 10

```

1: ATGTTATTTCTGTAAGCTCGACCAAGLMAAGTGGCAAGCAATTTGAGGATTACAAAGAC
60: -----
  M H F G F L D Q Q S A T T I L E D Y K N
2: ATGACCAACATCGCGTAGCTATCTTGGCTACGGAAAGCTGGGACCCAGCGTCGAAAG
120: -----
  H T N I F V A I V G Y C H I C R S V E K
3: CTTATTGCCAAGCAGCCCGACATGGACCTTGTAGGAATCTTCTCGCGCCGCGCCACCCCTC
180: -----
  L I A K Q P D M D L V G I F S R R A T L
4: GACACAAAGACCCAGTCTTTGATGTGCGCGACCTGGACAAGCAGCCGACGCGTGGAG
240: -----
  D T K T P V F D V A D V D K H A D D V D
5: GTGCTGTTCTCTGTCATGGGCTCGCCACCCAGATCCCTGAGCAGGCACCAAGTTCCGG
300: -----
  V L F L C H G S A T O I P E Q A P K F A
6: CAGTTCGCGCTGCACCGTAGACACCTACGACACCCAGCCGACATCCCAAGCCACCGCCAG
360: -----
  Q F A C T V D T Y D N H R D I P R H R Q
7: GTCATGAACGAAGCGCCACCGCAGCGCGCAACGTTGCACTGGTCTCTACCGGCTGGGAT
420: -----
  V M N E A A T A A C N V A L V S T G W D
8: CCAGGAATGTTCTCCATCAACCGCGTGTACGAGCGGCAGTCTTAGCCGAGACCCAGCAG
480: -----
  P G H F S I N R V Y A A A V L A E H O Q
9: CACACCTTCTGGGGCCAGGTTTGTACAGGGCCACTCCGATGCTTTGCCAGGCATCCCT
540: -----
  H T F H G P G L S Q G H S D A L R P T P
10: GGCATTCTAAAGGCGCTCCAGTACACCTTCCCATCCCAAGAAGCCCTGGCAAGCGCCCG
600: -----
  C V Q K A V Q Y T L P S E E A L E H A R
11: CGTGGGAAGCCGCGCAGCTACCGGAAGGCAAAACGACAAAGCCCAATGTTCTGTTGGTT
660: -----
  R G E A G D L T G K Q T H K R O C F V V
12: CCGGACCGCGCGGAGCAGGAGCCCATCGAAGGACATCCGACCATCCCTGATTACTTC
720: -----
  A D A A D H E R I E N D I R T H F D Y F
13: GTTGGCTACGAAGTCGAAGTCAACTTCATCGACGAGCAACCTTGGACGCTGAGCAGACCC
780: -----
  V G Y E V E V N F I D E A T L D A E H T
14: GGCAAGCCACACGGCGGACAGTGATACCCACCGCGGACACCGGTGGCTTAACCCACACC
840: -----
  G M P H G G H V I T T C D T G C F N H T
15: GTGGAAATACATCTGAAGCTGGACCGAAGCCAGATTTACCGCTTCTTACAGATCCCT
900: -----
  V E Y I L K L D R N P D F T A S S Q I A
16: TTGGGTCGCGCAGCTACCCCATCAAGCAGCAGGGCCAAAGCGGTGCTTACCCGTCTCT

```

Fig 11A

008277-11122260

SEQ ID NO:10  
(cont)

```
901 ----- 960
      F G R A A H R M K Q Q C Q S G A F C Y L
      GAAGTTGCTCCATACCTGCTCTCCCCGGAAGAACTTGGATGATCTGATCGCACCGACGTC
961 ----- 1020
      E V A P Y L L S P E N L D D L I A P D V
      TAA
1021 --- 1023
```

Fig. 11B

008211-14422/60

Sequence of full length *lysA* from NRRL B-11474 (SEQ ID NO: 11); Underlined region: the priming site for *lysA* primer

ATGGCTACAGTTGAAAAATTTCAATGAACCTCCCGCACACGTATGGCCACGCAATGCAGTG  
CGCCAAGAAGACGGCGTTGTACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA  
TACGGAACCCCACTGTTGCTAGTCGACGAGGACGATTTCCGTTCCCGCTGTCCGACATG  
GCTACCGCATTCGGTGGACCAAGCAATGTGCACTACGCATCCAAAGCGTTCCCTGACCAAG  
ACCATTTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCGTCCATCAATGAA  
CTGGGCATTCGCCCTGGCCGCTGGTTTCCCGGCCAGCCGTATCACCGCGCACGGCAACCAAC  
AAAGGCGTAGAGTTCTGCCGCCGTTGGTTCAAAACCGGTGTCCGGCATGTGGTGTGGAC  
TCCGCGCAGGAATTGGAACTGCTGGATTACGTTGCCGCTGGTGAAGGCAGATCCAGGAC  
GTGTTGATCCCGCTGAAGCCAGGTATCGAAGCCCAACCCACGAGTTCATCGCCACTAGC  
CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCCGCATTCGAAGCAGCGAAA  
GCAGCCAACAATGCAGAGAACCTGAACCTGGTTGGTCTGCACCTGCCATGTTGGTTCCAG  
GTGTTTCGACGCGCGAAGGCTTCAAGCTGGCAGCAGAGCGCGTGTGGGCTGTACTCAACAG  
ATCCACAGCGAACTAGGTGTGCGCCCTTCCTGAGCTGGACCTCGGTGGCGGATACGGCATC  
GCCTACACTGCAGATGAGGAACCACTCAACGTCGCAGAGTCCGCTCCGACCTACTCACC  
GCAGTCGGAAAAATGGCAGCGGAACCTAGGCATCGACCGCACCAACCGTGCTTGTGAGCCC  
GGCCGCGCTATCCGACGGCCCTCCACCGTGACCATCTACGAAGTCCGGCACCACCAAAAAC  
GTCCACGTAGACGACGACAAAACCCGCGCTACGTAGCCGTCGACGGAGGCATGTCCGAC  
AACATCCGCCCAGCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC  
GAAGGAGACCCAGTAAGCACCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG  
ATCAACGATGAAATCTACCCATCTGACATCACCAGCGCGGACTTCCTCGCACTCGCAGCC  
ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCTTACACGCGCCCGCGCTC  
GTGTCCGTCGGCGCTGGCAGCTCCCGCTCATGCTGGCGCGGAAACCTCGACGACATC  
CTCTCACTAGAGGCATAA

Fig. 12

full length sequence of LysA (NRRL-B11474)  
DIAMINOPIMELATE DECARBOXYLASE (Lys A) SEQ ID NO:12

MATVENFNELEPAHVWFRNAVVRQEDGVVTVAGVFLPDLAEEYGTPLFVVDEDDFRSRCDM  
ATAFGGPGNVHYASKAFLTKTTARWVDEEGLALDIASINELGIALAAGFPASRITAHGNN  
KGVFELRALVQNGVGHVVLDSAQELLELDYVAAGEGKIQDVLIRVKPGIEARTHEFLATS  
HEDQKFGFSLASGSFAFEAKAANNAENLNVLGLHCHVGSQVFDAGFKLAAERVVLGLYSQ  
IHSELGVALPELDLGGGYGIAYTADDEFLNVAEVASDLLTAVGKMAELGIDAPTVLVEP  
GRAIAGPSTVTIYEVGTTKNVHVDDDKTIRRYVAVDGGMSDNIRPALYGYSEYDARVVSRA  
EGDPVSTRIVGSHCESGDILINDEIYPSDITSGDFLALAATGAYCYAMSSRYNAFTRPAV  
VSVRAGSSRLMLRRETLDLILSLEA

Fig. 13



Nucleotide

sequences of AS019 lysA (SEQ ID NO:13) (p 2S6)

```

1  ATGGCTACAG TTGAAAATTT CAATGAACTT CCGGCACACG TATGGCCACG
51  CAATGCCGTG CGCCAAGAGG ACGGCTTTGT CACCGTCGCT GGTGTGCCTC
101 TGCCTGACCT CGCTGAAGAA TACGGACACC CACTGTTTCGT AGTCGACGAG
151 GACGATTTCC GTTCCCGCTG TCGCGACATG GCTACCGCAT TCGGTGGACC
201 AGGCAATGTG CACTACGCAT CTAAAGCGTT CCTGACCAAG ACCATTGCAC
251 GTTGGGTTGA TGAAGAGGGG CTGGCACTGG ACATTGCATC CATCAACGAA
301 CTGGGCATTG CCCTGGCCGC TGGTTTCCCC GCCAGCCGTA TCACCGCGCA
351 CGGCAACAAC AAAGGCGTAG AGTTCCTGCG CGCGTTGGTT CAAAACGGTG
401 TGGGACACGT GGTGCTGGAC TCCGCACAGG AACTAGAACT GTTGGATTAC
451 GTTGGCCGTG GTGAAGGCAA GATTCAGGAC GTGTGATCC GCGTAAAGCC
501 AGGCATCGAA GCACACACCC ACGAGTTCAT CGCCACTAGC CACGAAGACC
551 AGAAGTTCCG ATTCTCCCTG GCATCCGTT CCGCATTCGA AGCAGCAAAA
601 GCCGCCAACA ACGCAGAAAA CCTGAACCTG GTTGGCCTGC ACTGCCACGT
651 TGGTTCCCAG GTGTTGACG CCGAAGSCTT CAAGCTGGCA GCAGAACGCG
701 TGTGGGCCT GTACTCACAG ATCCACAGCG AACTGGGCGT TGCCCTTCCT
751 GAACTGGATC TCGGTGGCGG ATACGTCATT GCCTATACCG CAGCTGAAGA
801 ACCACTCAAC GTGCGAGAAG TTGCCGCCGA CCTGCTCACC GCAGTCGGAA
851 AAATGGCAGC GGAAC TAGGC ATCGACGCAC CAACCGTGCT TGTGAGCCC
901 GGCCGCGCTA TCGCAGGCC CTCCACCGTG ACCATCTACG AAGTCGGCAC
951 CACCAAGAC GTCCACGTAG ACGACGACAA AACC CGCCGT TACATCGCCG
1001 TGGACGGAGG CATGTCCGAC AACATCCGCC CAGCACTCTA CGGCTCCGAA
1051 TACGACGCCC GCGTAGTATC CCGCTTCGCC GAAGGAGACC CAGTAAGCAC
1101 CCGCATCGTG GGCTCCCACT GCGAATCCGG CGATATCCTG ATCAACGATG
1151 AAATCTACCC ATCTGACATC ACCAGTGGCG ACTTCCTTGC ACTCGCAGCC
1201 ACCGGCGCAT ACTGCTACGC CATGAGCTCC CGCTACAACG CCTTCACACC
1251 GCCCGCCGTC GTGTCCGTCC GCGCTGGCAG CTCCCGCCTC ATGCTGCGCC
1301 GCGAAACGCT CGACGACATC CTCTCACTAG AGGCATAA

```

Fig. 14

008211 " F4422/60

Seq ID NO: 14 Full length amino acid sequence of LysA (pRS6)

```

1  ATGGCTACAGTTGAAAATTTCAATGAAGTTCCCGCACACGTATGGCCACGCCATGGCCGTG  60
   M A T V E N F N E L P A H V W P R N A V
61  CGCCAAGAAGACGGCGTTGTCACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA  120
   R Q E D G V V T V A G V P L P D L A E E
121 TACGGAACCCCACTGTTCTAGTCGACGAGGACGATTCCGTTCCCGCTGTCGCGACATG  180
   Y G T P L F V V D E D D F R S R C R D M
181 GCTACCGCATTTCGGTGGACCAGGCAATGTGCACTACGCATCTAAAGCGTTCCTGACCAAG  240
   A T A F G G P G N V H Y A S K A F L T K
241 ACCATTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCATCCATCAACGAA  300
   T I A R W V D E E G L A L D I A S I N E
301 CTGGGCATTGCCCTGGCCGCTGGTTTCCCCGCCAGCCGTATCACCGCGCACGGCAACAAC  360
   L G I A L A A G F P A S R I T A H G N N
361 AAAGGCGTAGAGTTCTCTGCGCGCTGGTTCAAAACGGTGTGGGACACGTGGTGTCTGGAC  420
   K G V E F L R A L V Q N G V G H V V L D
421 TCCGCACAGGAAGTAGAACTGTTGGATTACGTTGCCGCTGGTGAAGGCAAGATTACGGAC  480
   S A Q E L E L L D Y V A A G E G K I Q D
481 GTGTTGATCCGCGTAAAGCCAGGCATCGAAGCACACCCACGAGTTCATCGCCACTAGC  540
   V L I R V K P G I E A H T H E F I A T S
541 CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCGCGATTGGAAGCAGCAAAA  600
   H E D Q K F G F S L A S G S A F E A A K
601 GCCGCCAACAACGCAGAAAACCTGAACCTGGTTGGCCTGCACTGCCACGTTGGTTCCCAG  660
   A A N N A E N L N L V G L H C H V G S Q

```

Fig 15A

0022441.12200

SEQ ID NO: 14 Lys A (pRS6)  
(cont.)

```

661  GTGTTTCGACGCCGAAGGCTTCAAGCTGGCAGCAGAACGCGTGTGGGCCTGTACTCACAG
-----+-----+-----+-----+-----+-----+-----+-----+ 720
      V F D A E G F K L A A E R V L G L Y S Q
      ATCCACACCGAACTGGGCGTTGCCCTTCTGAACTGGATCTCGGTGGCGGATACGGCATT
721  -----+-----+-----+-----+-----+-----+-----+ 780
      I H S E L G V A L P E L D L G G G Y G I.
      GCCTATACCGCAGCTGAAGAACCCTCAACGTCGCAGAAGTTGCCTCCGACCTGCTCACC
781  -----+-----+-----+-----+-----+-----+-----+ 840
      A Y T A A E E F L N V A E V A S D L L T
      GCAGTCGGAAAAATGGCAGCGGAAGTGGCATCGACGCACCAACCGTGCTTGTGAGCCC
841  -----+-----+-----+-----+-----+-----+-----+ 900
      A V G K M A A E L G I D A R T V L V E P
      GGCCGCGCTATCGCAGGCCCTCCACCGTGACCATCTACGAAGTCGGCACCACCAAAGAC
901  -----+-----+-----+-----+-----+-----+-----+ 960
      G R A I A G P S T V T I Y E V G T T K D
      GTCCACGTAGACGACGACAAAACCCGCCGTTACATCGCCGTGGACGGAGGCATGTCCGAC
961  -----+-----+-----+-----+-----+-----+-----+ 1020
      V H V D D D K T R R Y I A V D G G M S D
      AACATCCGCCCAGCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
      N I R P A L Y G S E Y D A R V V S R F A
      GAAGGAGACCCAGTAAGCACCCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
      E G D P V S T R I V G S H C E S G D I L
      ATCAACGATGAAATCTACCCATCTGACATCACCAGCGGCGACTTCCTTGCACTCGCAGCC
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
      I N D E I Y P S D I T S G D F L A L A A
      ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCTTCACACGGCCCGCCGTC
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
      T G A Y C Y A M S S R Y N A F T R P A V
      GTGTCCGTCCGCGCTGGCAGCTCCCGCTCATGCTGCGCCGCGAAACGCTCGACGACATC
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
      V S V R A G S S R L M L R R E T L D D I

```

Fig 15B

09722441.11800

[illegible]

Fig 15C

Nucleotide. sequence of orf2 in dapBA operon SEQ ID NO: 15

```

1 GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTTT
51 TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GGCGCGGAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAACTTT TGATAAGCCG
151 AACCCTCGAA CTGCTTCCAA TGCTGCGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCAA TGCCACGATG TATATCCGAG
251 GCATTTCTCG GTCCGCGACC CATGAATTGG TCCGACACCG CCATTTTTC
301 TTCTCTCAAC TGTCTCAGCG TTTCGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCACT CTCATCGATG AAGATCCGCA GTTGCCTGAA CTTTTCATGC
401 ACGCCATGGA TGAGTCTCGG TTCGCTTTCA ATGAGCTGCT TAATGCGCTG
451 GAAGAAAAAC TTGGCGATGA ACCGAATGCA CTTTAAAGGA AAAAGCAGGC
501 TCGTCAAGCA GCTCGCGCTG TGCTGCCCAA CGCTACAGAG TCCAGAATCG
551 TGGTGTCTGG AAACCTCCGC ACCTGGAGGC ATTCATTGG CATGCGAGCC
601 AGTGAACATG CAGACGTCGA AATCCGCGAA GTACCGGTAG GATGTTTAAG
651 AAAGCTGCAG GTAGCAGCGC CAACTGTTTT CGGTGATTTT GAGATTGAAA
701 CTTTGGCAGA CGGATCGCAA ATGGCAACAA GCCCGTATGT CATGGACTTT
751 TAA

```

Fig 1b

SEQ ID No: 16

ORF2 amino acid sequence

```

1  GTGGCCGAACAAGTTAAATTGAGCGTGCAGTTGATAGCGTGCAGTTCTTTTACTCCACCC
   -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
   M A E Q V K L S V E L I A C S S F T P
61  GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCGAGTTTGCGGGT
   -----+-----+-----+-----+-----+-----+-----+-----+ 120
   A D V E W S T D V E G A E A L V E F A G
121 CGTGCCTGCTACGAACTTTTGATAAGCCGAACCTCGAACTGCTTCCAATGCTGCGTAT
   -----+-----+-----+-----+-----+-----+-----+-----+ 180
   R A C Y E T F D K P N P R T A S N A A Y
181 CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG
   -----+-----+-----+-----+-----+-----+-----+-----+ 240
   L R H I M E V G H T A L L E H A N A T M
241 TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTTC
   -----+-----+-----+-----+-----+-----+-----+-----+ 300
   Y I R G I S R S A T H E L V R H R H F S
301 TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT
   -----+-----+-----+-----+-----+-----+-----+-----+ 360
   F S Q L S Q R F V H S G E S E V V V P T
361 CTCATCGATGAAGATCCGCGAGTTGCGTGAACCTTTTCATGCACGCCATGGATGAGTCTCGG
   -----+-----+-----+-----+-----+-----+-----+-----+ 420
   L I D E D P Q L R E L F M H A M D E S R
421 TTCGCTTTCAATGAGCTGCTTAATGCGCTGGAAGAAAACTTGGCGATGAACCGAATGCA
   -----+-----+-----+-----+-----+-----+-----+-----+ 480
   F A F N E L L N A L E E K L G D E P N A
481 CTTTTAAGGAAGAAGCAGGCTCGTCAAGCAGCTCGCGCTGTGCTGCCCAACGCTACAGAG
   -----+-----+-----+-----+-----+-----+-----+-----+ 540
   L L R K K Q A R Q A A R A V L P N A T E
541 TCCAGAATCGTGGTGTCTGAAACTTCCGCACCTGGAGGCATTTTCATTGGCATGCGAGCC
   -----+-----+-----+-----+-----+-----+-----+-----+ 600
   S R I V V S G N F R T W R H F I G M R A
601 AGTGAACATGCAGACGTCGAAATCCGCGAAGTAGCGGTAGGATGTTTAAGAAAGCTGCAG
   -----+-----+-----+-----+-----+-----+-----+-----+ 660
   S E H A D V E I R E V A V G C L R K L Q
661 GTAGCAGCGCCAACTGTTTTCGGTGATTTTGAGATTGAACTTTGGCAGACGGATCGCAA
   -----+-----+-----+-----+-----+-----+-----+-----+ 720
   V A A P T V F G D F E I E T L A D G S Q
721 ATGGCAACAAGCCCGTATGTCATGGACTTTTAA
   -----+-----+-----+-----+-----+-----+-----+-----+ 753
   M A T S P Y V M D F

```

fig 17

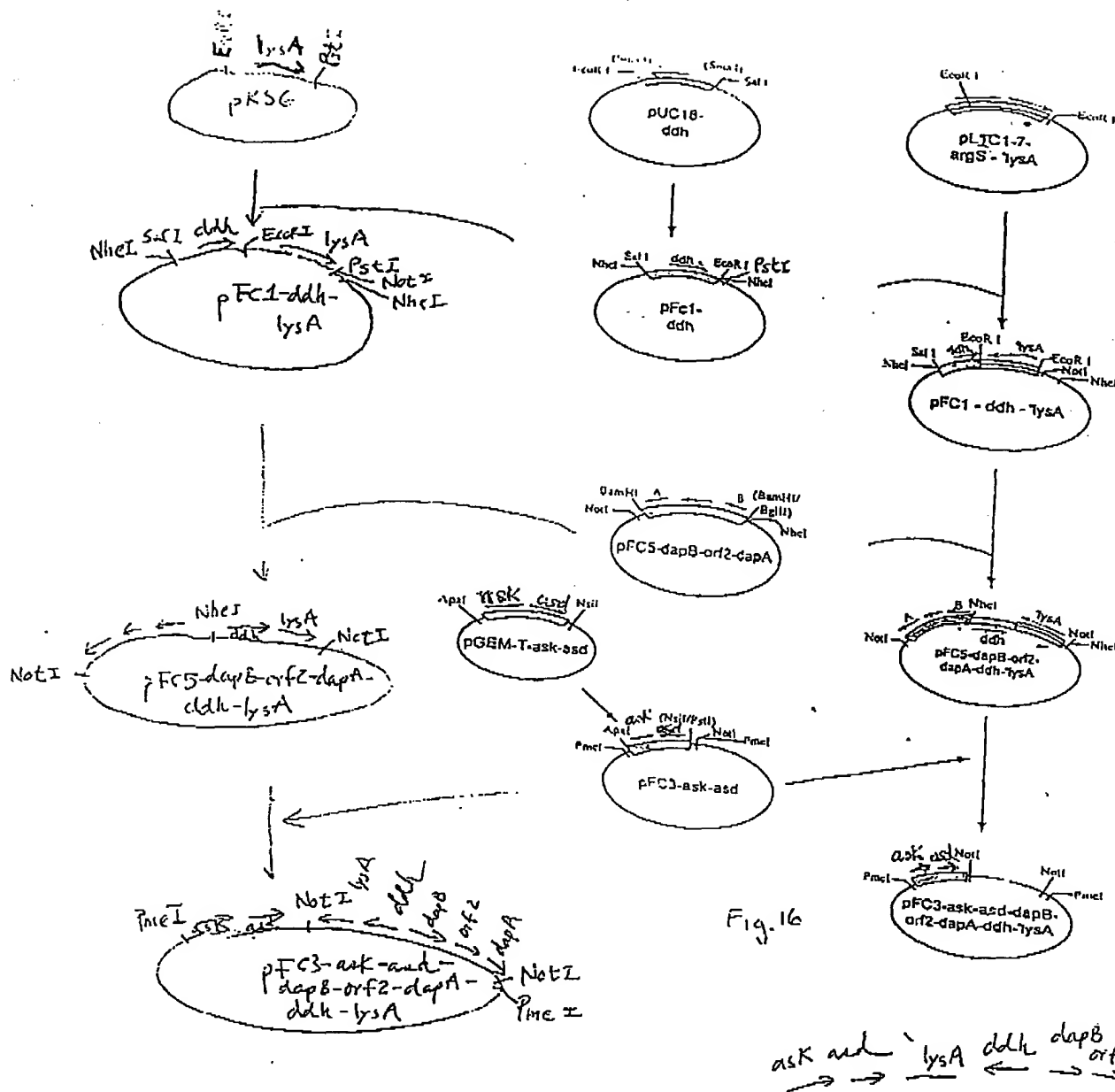


Fig. 18

ATCC 13032	1		50
N13			
ATCC 21529			
Consensus	HALVVQKYGG SSLESAERIR NVAERIVATK KAGNDVVVC SAMGDTTDEL		
	51		100
ATCC 13032			
N13			
ATCC 21529			
Consensus	LELAAAVNPV PPAREMDMLL TAGERISNAL VAMAIESLGA EAQSFQGSQA		
	101		150
ATCC 13032			
N13			
ATCC 21529			
Consensus	GVLTTTERHGN ARIVDVTPGR VREALDEGKI CIVAQFQGVN KETRDVTTLG		
	151		200
ATCC 13032			
N13			
ATCC 21529			
Consensus	RGGSDTTAVA LAAALNADVC EIYSODGVY TADPRIVPNA QZLEKLSFEE		
	201		250
ATCC 13032			
N13			
ATCC 21529			
Consensus	MLELAAVGSK ILVLRSEYA RAFNVPLRVR SSYSNDPQTL IAGSMEDIPV		
	251		300
ATCC 13032			
N13			
ATCC 21529			
Consensus	EEAVLTGVAT DKSEAKTVL GISDKPGEAA KVFRALADAE INIDMVLQNV		
	301		350
ATCC 13032		S	G
N13		A	D
ATCC 21529		A	G
Consensus	SSVEDGTTDI TFTCPRADGR RAKELKKLQ VQGNWTVLY DQVGEVSLV		
	351		400
ATCC 13032		T	
N13		T	
ATCC 21529		I	
Consensus	GAGNKSHPGV TAEFMEALRD VVNIELIST SEIRISVLIR EDDLDAARA		
	401	421	
ATCC 13032			
N13			
ATCC 21529			
Consensus	LHEQFQLGGE DEAVVYACTG R		

Fig. 19





# Making pFC2-ddh-lysA

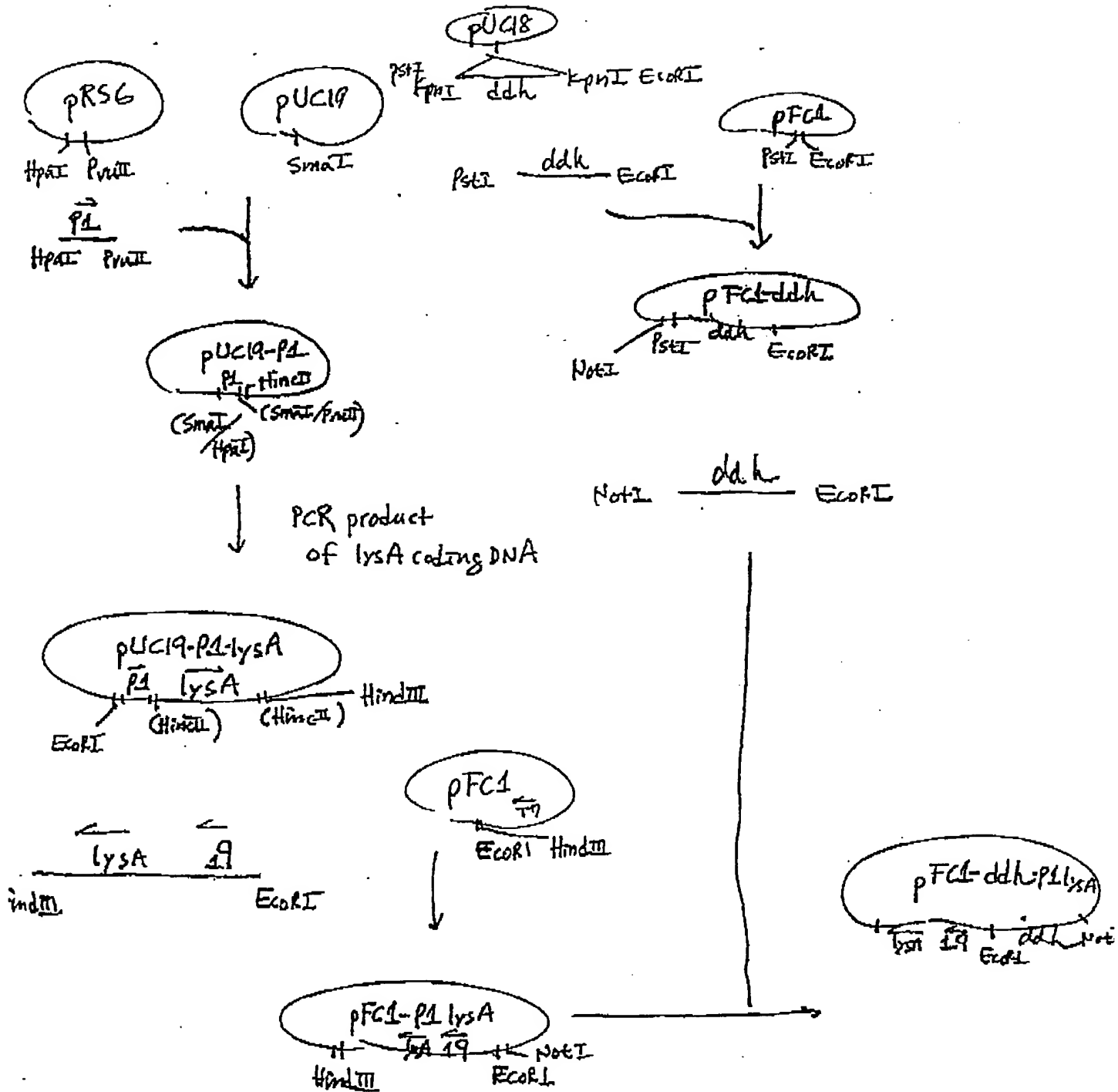


Fig. 21A

# Making pDELia2-KDABHP1L

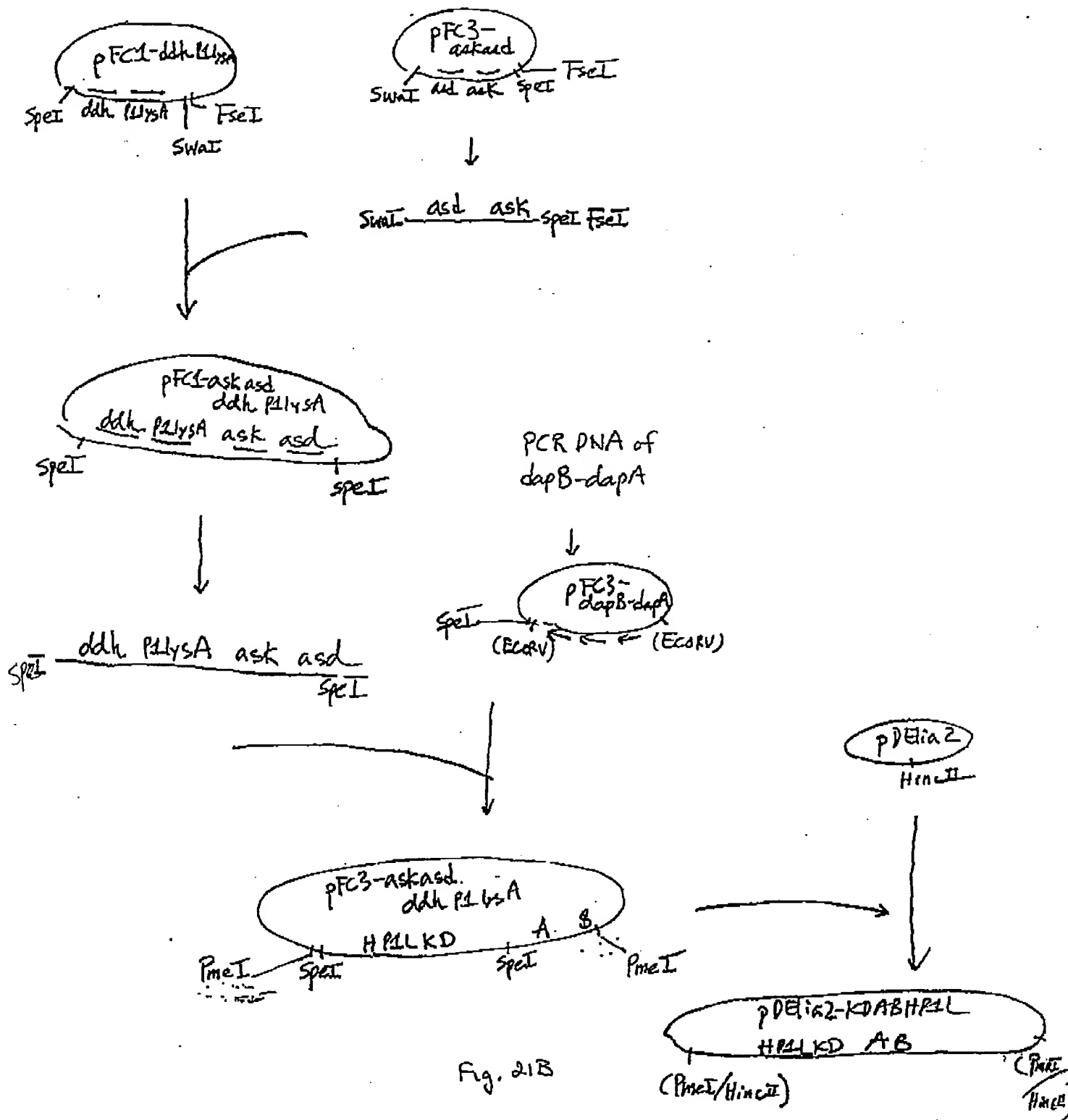


Fig. 21B

000211-11122260

# Making pDEla2Fc5-KDBHL

(-from Fig 16)

PCR: DNA  
of dapB-dapA

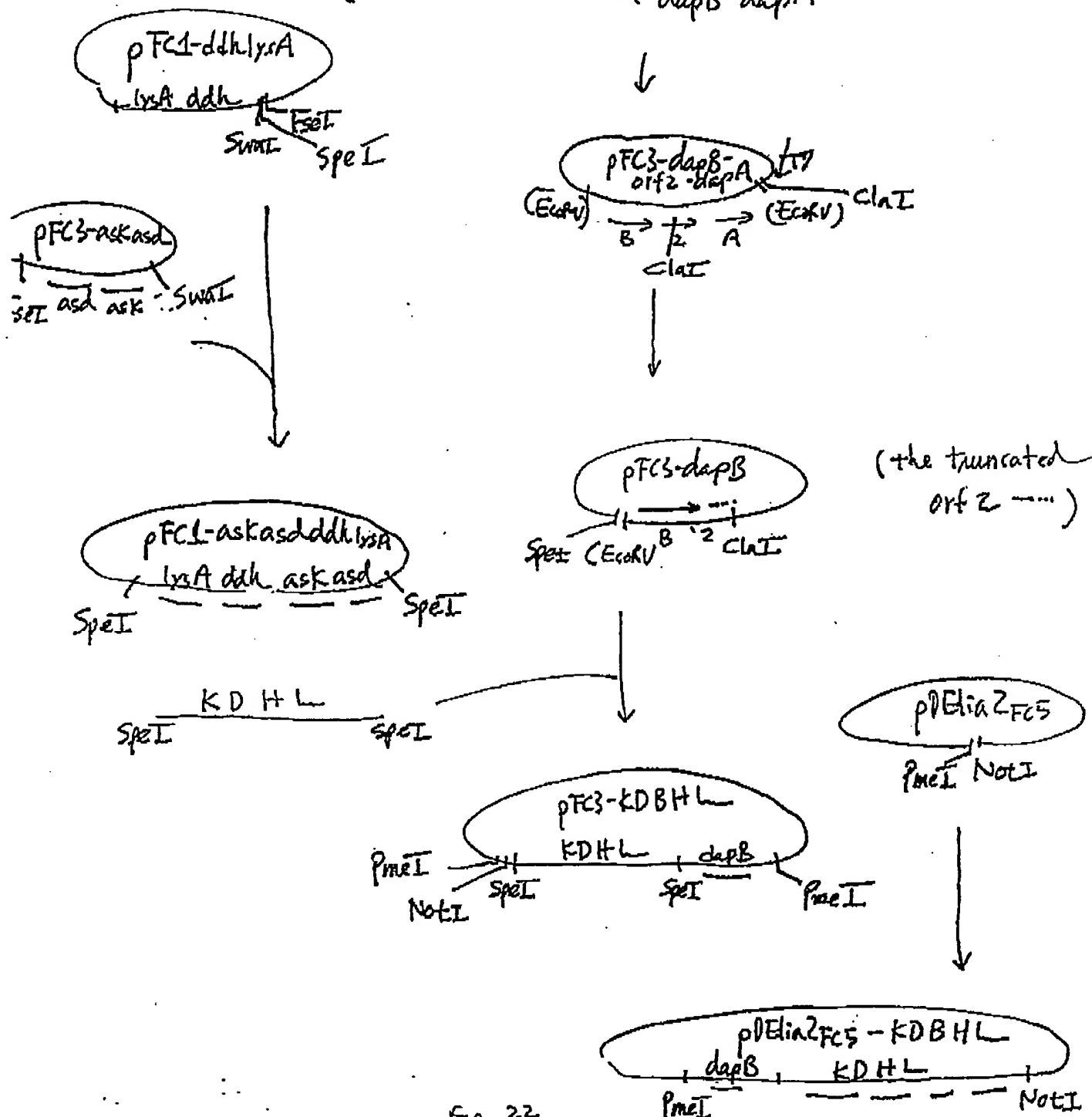


Fig. 22

orientation:  $\leftarrow B \quad \leftarrow D \quad \leftarrow K \quad \leftarrow H \quad \leftarrow L$

nucleotide sequence of truncated ORF2

SEK ID NO: 18

```
1  GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTTT
51  TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GGCGCGGAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAACTTT TGATAAGCCG
151 AACCCTCGAA CTGCTTCCAA TGCTGCGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCAA TGCCACGATG TATATCCGAG
251 GCATTTCTCG GTCGCGGACC CATGAATTGG TCCGACACCG CCATTTTTC
301 TTCTCTCAAC TGTCTCAGCG TTCGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCACT CTCAT
```

Fig. 23

008277-112800

SEQ. ID. NO: 19

Truncated ORF2

amino acid sequence

```

1  GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC
   -----+-----+-----+-----+-----+-----+-----+-----+ 60
   M A E Q V K L S V E L I A C S S F T P P
61  GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCCGAGTTTSCGGGT
   -----+-----+-----+-----+-----+-----+-----+ 120
   A D V E W S T D V E G A E A L V E F A G
121 CGTGCCTGCTACGAAACTTTTGATAAGCCGAACCCCTCGAACTGCTTCCAATGCTGCGTAT
   -----+-----+-----+-----+-----+-----+-----+ 180
   R A C Y E T F D K P N P R T A S N A A Y
181 CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG
   -----+-----+-----+-----+-----+-----+-----+ 240
   L R H I M E V G H T A L L E H A N A T M
241 TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTTC
   -----+-----+-----+-----+-----+-----+-----+ 300
   Y I R G I S R S A T H E L V R H R H F S
301 TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT
   -----+-----+-----+-----+-----+-----+-----+ 360
   F S Q L S Q R F V H S G E S E V V V P T
361 CTCAT ...
   -----
   L (1)

```

fig. 24

003211-1422/60

Seq ID No: 20

Sequence of truncated Lys A (Lys A)

(NRRL-B11474)

ATGGCTACAGTTGAAAATTTCAATGAACTTCCCGCACACGTATGGCCACGCAATGCAGTG  
CGCCAGAAGACGGCGTTGTCACCGTCGCTGGTGTGCCCTCTGCTGACCTCGCTGAAGAA  
TACGGAACCCCACTGTTGCTAGTCGACGAGGACGATTTCCTTCCCCTGTCCGACATG  
GCTACCGCATTCGGTGGACCAAGCAATGTGCACTACGCATCCAAAGCGTTCCTGACCAAG  
ACCATTCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCGTCCATCAATGAA  
CTGGGCATTCGCTGGCCGCTGGTTTCCCCGCCAGCCGTATCACCGCGCACGGCAACAC  
AAAGGCGTAGAGTTCTCTGCGCGCGTTGGTTCAAAACGCTGTGCGGCATGTGGTGTCTGGAC  
TCCGCGCAGGAATTGGAACCTGCTGGATTACGTTGCCGCTGGTGAAGGCAAGATCCAGGAC  
GTGTTGATCCGCGTGAAGCCAGGTATCGAAGCCACACCCACGAGTTCATCGCCACTAGC  
CACGAAGACCAGAAGTTCCGATTCTCCCTGGCATCCGGTTCCGCATTGAAGCAGCGAAA  
GCAGCCAAACAATGCAGAGAACTTGAACCTGGTTGGTCTGCACTGCCATGTTGGTTCCAG  
GTGTTGACGCCGAAGGCTTCAAGCTGGCAGCAGAGCGGTGTTGGGCTGTACTCACAG  
ATCCACAGCGAACTAGGTGTGCGCCCTTCTGAGCTGGACCTCGGTGGCGGATACGGCATC  
GCCTACACTGCAGATGAGGAACCACTCAACGTCGCAGAAGTCGCCTCCGACCT.

Fig. 25

Truncated sequence of LysA (NRRL-B11474).

DIAMINOPIMELATE DECARBOXYLASE (Lys A) SEQ ID NO: 21

MATVENFNELPAHVWPRNAVVRQEDGVVTVAGVPLDAAEYGTPLFVDEDDFRSRCRM  
ATAFGGGPGNVHYASKAFLTKTIARWVDEEGLALDIASINELGIALAAGFEASRITAHGNN  
KGVEFLRALVQNGVGHVVLDSAQEILELLDYVAAGEGKIQDVLRVKPGIEATHEFIATS  
HEDQKFGFSLASGSFAFEAAKAANNAENLNVLVGLHCHVGSQVDAEGFKLAASRVLGLYSQ  
IHSELGVALPELDLGGGYGIATYTADEEPLNVAEVASDL

Fig. 26

000217-11474-60